

TOP PAGE QUERY RESULTS PROJECTS VIEWS DATABANKS (III) View * Complete entries * DDBJRELEASE:AE015074 This entry is from: **DDBJRELEASE** LOCUS AE015074 10085 bp DNA linear BCT 18-0CT-2002 DEFINITION Shigella flexneri 2a str. 301 section 37 of 412 of the complete Save **ACCESSION** AE015074 AE005674 Link **VERSION** AE015074.1 **KEYWORDS** Launch SOURCE Shigella flexneri 2a str. 301 NClustalW ORGANISM Shigella flexneri 2a str. 301 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella. Printer Friendly REFERENCE (bases 1 to 10085) **AUTHORS** Jin, Q., Yuan, Z.H., Xu, J.G., Wang, Y., Shen, Y., Lu, W.C., Wang, J.H., Liu, H., Yang, J., Yang, F., Qu, D., Zhang, X.B., Zhang, J.Y., Yang, G.W., Wu, H. T., Dong, J., Sun, L. L., Xue, Y., Zhao, A. L., Gao, Y. S., Zhu, J. P., Kan, B., Chen, S. X., Yao, Z. J., He, B. K., Chen, R. S., Ma, D. L., Qiang, B. Q., Wen, Y. M., Hou, Y. D. and Yu, J. TITLE Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157 JOURNAL Nucleic Acids Res. 30 (20), 4432-4441 (2002) **PUBMED** 12384590 REFERENCE 2 (bases 1 to 10085) **AUTHORS** Jin, Q., Shen, Y., Wang, J.H., Liu, H., Yang, J., Yang, F., Zhang, X.B., Zhang, J. Y., Yang, G.W., Wu, H. T., Dong, J., Sun, L.L., Xue, Y., Zhao, A. L., Gao, Y. S., Zhu, J. P., Chen, S. X., Yao, Z. J., Wang, Y., Lu, W. C., Qiang, B. Q., Wen, Y. M. and Hou, Y. D. TITLE Direct Submission **JOURNAL** Submitted (08-MAY-2001) Microbial Genome Center of Chinese Ministry of Public Health, 100 YingXin Jie, XuanWu Qu, Beijing 100052, P.R. China **FEATURES** Location/Qualifiers 1..10085 source /organism="Shigella flexneri 2a str. 301" /strain="301" /serotype="2a" /db_xref="taxon:198214" 91..795 gene /gene="adk" /note="SF0419" 91..795 CDS /gene="adk" /note="Residues 2 to 234 of 234 are 98 pct identical to residues 1 to 233 of a 233 aa protein from Escherichia coli gb: AAB40228.1' /codon_start=1 /transl_table=11 /product="adenylate kinase" /protein_id="AAN42074.1' /db_xref="G1:24050653" /translation="MVVSFIAFSKKSTHFKGIFAMRIILLGAPGAGKGTQAQFIMEKY GIPQISTGDMLRAAVKSGSELGKQAKDIMDAGKLVTDELVIALVKERIAQEDCRNGFL LDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDRIVGRRVHAPSGRVYHVKFNPP KVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMTAPLIGYYSKEAEAGNTKYAKVDG TKQVAEVRADLEKILG" 927..1889 gene /gene="hemH' /note="SF0420" <u>CDS</u> 927..1889 /gene="hemH" /note="Residues 1 to 320 of 320 are 98 pct identical to residues 1 to 320 of a 320 aa protein from Escherichia

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